

CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-141-645-1

Query Match Similarity 88.7%; Score 102; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.2e-06; Mismatches 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GICRCICTRGRCRGR 18
Db 1 GICRCICGRCIGR 18

RESULT 3
US-10-141-645-2

Sequence 2, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
; US-10-141-645-2

Query Match Similarity 86.1%; Score 99; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 2e-05; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GICRCICTRGRCRGR 18
Db 1 GICRCICGRCIGR 18

RESULT 4
US-10-141-645-3

Sequence 3, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SBQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
; US-10-141-645-4

Query Match Similarity 84.3%; Score 97; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.4e-05; Mismatches 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GICRCICTRGRCRGR 18
Db 1 GICRCICGRCIGR 18

RESULT 5
US-10-141-645-4

Sequence 4, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; FILE REFERENCE: UCLA-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SBQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic variant
; US-10-141-645-4

Query Match Similarity 84.3%; Score 97; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.4e-05; Mismatches 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GICRCICTRGRCRGR 18
Db 1 GICRCICGRCIGR 18

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; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: synthetic variant
; US-10-141-645-5

Query Match 84.3%; Score 97; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.4e-05; Matches 15; Conservatve 0; Mismatches 3; Indels 0; Gaps 0;
Db 1 GICRCICTRGFCRCICGR 18

RESULT 7
US-10-141-645-7
; Sequence 7, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCL-A-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE: OTHER INFORMATION: synthetic variant
; US-10-141-645-7

Query Match 82.6%; Score 95; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.7e-05; Matches 15; Conservatve 0; Mismatches 3; Indels 0; Gaps 0;
Db 1 GICRCICTRGFCRCICGR 18

RESULT 8
US-09-309-487-1
; Sequence 1, Application US/09309487
; Patent No. 6335318
; GENERAL INFORMATION:
; APPLICANT: Michael E. Selsted
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/309,487
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US/09/309,487
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
; US-09-309-487-1

Query Match 76.5%; Score 88; DB 3; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.00036; Matches 13; Conservatve 1; Mismatches 4; Indels 0; Gaps 0;
Db 1 GICRCICTRGFCRCICGR 18

RESULT 9
US-09-967-808-1
; Sequence 1, Application US/09967808
; Patent No. 6314727
; GENERAL INFORMATION:
; APPLICANT: Michael E. Selsted
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Yuan, Jun
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/967,808
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US/09/309,487
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
; US-09-967-808-1

Query Match 76.5%; Score 88; DB 4; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.00036; Matches 13; Conservatve 1; Mismatches 4; Indels 0; Gaps 0;
Db 1 GICRCICTRGFCRCICGR 18

RESULT 10
US-10-141-645-8
; Sequence 8, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCL-A-001CIP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18

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; TYPE: PRT ; LENGTH: 18
; ORGANISM: Artificial Sequence ; TYPE: PRT
; FEATURE: ; ORGANISM: Macaca mulatta
; OTHER INFORMATION: Synthetic variant ; US-09-917-340-53

US-10-141-645-8
Query Match 75.7%; Score 87; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 0.00046; 0; Mismatches 4; Indels 0; Gaps 0;
Matches 14; Conservative 1; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCRCIGR 18
Db 1 GICICIGGYGICRCIGR 18

RESULT 11
US-10-141-645-9
; Sequence 9, Application US/10141645
; Patent No. 6713078
; GENERAL INFORMATION:
; APPLICANT: Robert Lehrer
; APPLICANT: Alan Waring
; APPLICANT: Alexander Cole
; APPLICANT: Teresa Hong
; TITLE OF INVENTION: Retrocyclins - Antiviral and
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: UCL-A-001CP
; CURRENT APPLICATION NUMBER: US/10/141,645
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/284,855
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: Unassigned
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic variant
; US-10-141-645-9

RESULT 12
Query Match 75.7%; Score 87; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 0.00046; 0; Mismatches 4; Indels 0; Gaps 0;
Matches 14; Conservative 1; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCRCIGR 18
Db 1 GICICICORGICYCICGR 18

RESULT 13
US-09-309-487-9
; Sequence 9, Application US/09309487
; Patent No. 6335318
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/309,487
; CURRENT FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
; US-09-309-487-9

RESULT 14
Query Match 73.9%; Score 85; DB 3; Length 18;
Best Local Similarity 75.0%; Pred. No. 0.00078; 1; Mismatches 3; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCRCIC 16
Db 3 GFCRCICRRGFCRCIC 18

RESULT 15
US-09-917-340-53
Query Match 74.8%; Score 86; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 0.0006; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RCICTRGFCRCIGR 18
Db 1 RCICTRGFCRCICR 15

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; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
; US-09-917-340-53

Query Match 74.8%; Score 86; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 0.0006; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RCICTRGFCRCIGR 18
Db 1 RCICTRGFCRCICR 15

RESULT 13
US-09-309-487-9
; Sequence 9, Application US/09309487
; Patent No. 6335318
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
; FILE REFERENCE: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/309,487
; CURRENT FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Macaca mulatta
; US-09-309-487-9

RESULT 14
Query Match 73.9%; Score 85; DB 3; Length 18;
Best Local Similarity 75.0%; Pred. No. 0.00078; 1; Mismatches 3; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCRCIC 16
Db 3 GFCRCICRRGFCRCIC 18

RESULT 15
US-09-917-340-53
Query Match 73.9%; Score 85; DB 4; Length 18;
Best Local Similarity 75.0%; Pred. No. 0.00078; 1; Mismatches 3; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCRCIC 16

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Db | |||:||| ||||| 18
3 GFCCRCLCRGGVCRIC

RESULT 15

US-09-309-487-21

Sequence 21, Application US/09309487

Patent No. 6333318

GENERAL INFORMATION:

APPLICANT: Selected, Michael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Yuan, Jun

APPLICANT: Ouellette, Andre J.

TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same

FILE REFERENCE: P-DC 3095

CURRENT APPLICATION NUMBER: US/09/309,487

CURRENT FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 21

LENGTH: 92

TYPE: PRT

ORGANISM: Macaca mulatta

US-09-309-487-21

Query Match 63.5%; Score 73; DB 3; Length 92;
Best Local Similarity 84.6%; Pred. No. 0.064;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 4 RCICTRGFCRCIC 16
Db 65 RCICTRGFCRLC 77

Search completed: March 22, 2005, 20:51:17
Job time : 43 secs

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XX OS Synthetic.
 XX Homo sapiens.
 XX PN WO2004033479-A2.
 XX
 PD 22-APR-2004.
 XX PP 06-MAY-2003; 2003WO-US014106.
 XX PR 06-MAY-2002; 2002US-00141645.
 XX PA (REGC) UNIV CALIFORNIA.
 PA (LEHR) LEHRER R I.
 PA (WARI) WARING A J.
 PA (COLE) COLE A M.
 PA (HONG) HONG T B.
 XX PT Lehrer RI, Waring AJ, Cole AM, Hong TB;
 XX DR WPI; 2004-340893/31.
 XX DR N-PSDB; ADN08193.
 XX PT New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections.
 PT XX PS Claim 9; SEQ ID NO 1; 82pp; English.
 CC The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide; an isolated nucleic acid encoding a primate retrocyclin; a method for preventing retroviral infection in a cell by administering an effective dose of a circular minidefensin or retrocyclin to the cell; a method for killing microbial organisms by administering an effective dose of retrocyclin to the microbial organisms; a method for administering retrocyclin as a therapeutic agent to a patient with an established microbial or viral infection; and a method for administering retrocyclin as a prophylactic agent to prevent a microbial or viral infection in a patient at risk of developing such infection. The retrocyclin peptide has antibacterial and virucide activities. The retrocyclin peptide can be used as a vaccine and can be used in immunotherapy. The peptide and polypeptides are useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections. This sequence represents a retrocyclin peptide of the invention.
 CC SQ Sequence 18 AA:
 Query Match 88.7%; Score 102; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 0.0044;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 GICRCIICTRGRFCICGR 18
 Db 1 GICRCIICGRCICGR 18
 RESULT 13
 ID ABP53298 standard; peptide: 18 AA.
 AC ABP53298;
 XX AC ABP53298;
 XX DT 13-NOV-2002 (first entry)
 XX DE Anti-viral chimeric theta defensin peptide H/RTD-3 SEQ ID NO:31.
 XX KW anti-viral; viral infection; theta-defensin; lipid environment;
 KW amphipathic alpha-helical structure; virucide; anti-HIV; immunisation;
 KW viral growth inhibitor; viral proliferation inhibitor.
 XX OS Homo sapiens.
 OS Macaca mulatta.

XX OS Synthetic.
 XX WO200260468-A2.
 XX PD 08-AUG-2002.
 XX PP 29-JAN-2002; 2002WO-US002435.
 XX PR 30-JAN-2001; 2001US-0265270P.
 XX PR 01-AUG-2001; 2001US-0309368P.
 XX PA (IOWA) UNIV IOWA RES FOUND.
 PA (IOWA) UNIV IOWA RES FOUND.
 PI Maury W, Stapleton J, Stinski M, Roller R, McCray PB, Tack B;
 XX DR WPI; 2002-674815/72.
 XX PT New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
 XX PS Disclosure: Page 10; 65pp; English.
 CC The present invention describes a method (M1) of using a first anti-viral peptide (1) comprising a theta-defensin peptide in an amphipathic alpha-helical structure in a lipid environment for reducing the infectivity of a virus. (1) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (1) can be used for inhibiting the growth and proliferation of a virus and so can be used for: (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling viral spread within a virally-infected subject (VS), reducing viral burden in a VS, reducing virus shed from a VS, reducing percentage of VS in a population regardless of viral infection status or inducing latency in a VS; (b) reducing the infectivity of a virus; and (c) rendering virus-contaminated tissue or fluid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (M1) is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered to a patient who is immunosuppressed or to a subject who is not infected with the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is chronically, latently or acutely infected with the virus. The present sequence represents a chimeric human/rhesus monkey theta defensin anti-viral peptide, which is given in the exemplification of the present invention.
 XX SQ Sequence 18 AA:
 Query Match 87.0%; Score 100; DB 5; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00071;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 GICRCIICTRGRFCICGR 18
 Db 1 GICRCIICRGVCICGR 18
 RESULT 14
 ID AAE33864 standard; peptide: 18 AA.
 AC AAE33864;
 XX AC AAE33864;
 XX DT 16-APR-2003 (first entry)
 XX DE Enantio-RC-101 retrocyclin peptide analogue.
 XX KW Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; KW human immunodeficiency virus; bacterial vaginosis; ophthalmic infection;

SQ sequence 18 AA;

Query Match 90.4%; Score 104; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.00027; Mismatches 0;

Matches 16; Conservative 0; Indels 0; Gaps 0;

XX viral growth inhibitor; viral proliferation inhibitor.

XX Macaca mulatta.

OS Synthetic.

OS

PN WO20260568-A2.

XX

PD 08-AUG-2002.

XX

PP 29-JAN-2002; 2002WO-US002435.

XX

PR 30-JUN-2001; 2001US-0265270P.

PR 01-AUG-2001; 2001US-030368P.

XX

PA (IOWA) UNIV IOWA RES FOUND.

XX

PI Maury W., Stapleton J., Stinski M., Roller R., McCray PB., Tack B., DR

XX

WPI, 2002-674815/72.

XX

PT New method of using a first anti-viral peptide comprising a Theta-

PT defensin Peptide in an amphipathic Alpha-helical structure in a lipid

PT environment for reducing the infectivity of a virus.

XX

PS Disclosure; Page 10; 65PP; English.

XX

CC The present invention describes a method (M1) of using a first anti-viral

CC peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-

CC helical structure in a lipid environment for reducing the infectivity of anti-

CC a virus. (I) can have virucide and anti-HIV activities and can be used

CC to reduce virus growth, infectivity burden, shed, and development of anti-

CC -viral resistance. (I) can be used for inhibiting the growth and

CC proliferation of a virus and so can be used for: (a) protecting or

CC treating subject from a viral infection, preventing recurrent viral

CC infection in a subject harbouring a latent virus, controlling virus

CC spread within a virally-infected subject (VS), reducing viral burden in a

CC VS, reducing virus shed from a VS reducing percentage of VS in a

CC population regardless of viral infection status, or inducing latency in a

CC VS; (b) reducing the infectivity of a virus; and (c) rendering the virus-

CC contaminated tissue or fluid sample safe for use, or reducing the number

CC of infectious virus particles in a population of viruses. (M1) is useful

CC for reducing the infectivity of a virus in sheep, cattle, horses, swine,

CC cats, fowl and humans e.g. an enveloped virus infecting humans such as

CC human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is

CC administered to a patient who is immunosuppressed or to a subject who is

CC not infected with the virus, where the first anti-viral peptide is

CC administered prior to or subsequent to the virus contacting the subject.

CC The anti-viral peptide is most preferably administered to a subject who

CC is chronically, latently or acutely infected with the virus. The present

CC sequence represents a rhesus monkey theta defensin anti-viral peptide,

CC which is given in the exemplification of the present invention.

XX

SQ sequence 18 AA;

Query Match 89.6%; Score 103; DB 4; Length 18;

Best Local Similarity 88.9%; Pred. No. 0.00035; Mismatches 2;

Matches 16; Conservative 0; Indels 0; Gaps 0;

XX

OY 1 GICRCICTRGFCRCIGR 18

Db 1 GFRCICITRGFCRCIGR 18

DB RESULT 7

ABP53295

ID ABP53295 standard; peptide; 18 AA.

XX

AC ABP53295;

XX

DT 13-NOV-2002 (first entry)

AC

DE Anti-viral theta defensin peptide RTD-2 SEQ ID NO:28.

XX

KW Anti-viral; viral infection; theta-defensin; lipid environment; amphyopathic alpha-helical structure; virucide; anti-HIV; immunation;

XX

CC infection; and a method for administering retrocyclin as a prophylactic
 CC agent to prevent a microbial or viral infection in a patient at risk of
 CC developing such infection. The retrocyclin peptide has antibacterial and
 CC virucide activities. The retrocyclin peptide can be used to treat a viral
 CC infection such as HIV-1. The retrocyclin peptide can be used as a vaccine
 CC and can be used in immunotherapy. The peptide and polypeptides are useful
 CC as therapeutic and prophylactic agents for treating and preventing
 CC microbial and viral infections. This sequence represents a retrocyclin
 CC peptide of the invention.

XX Sequence 18 AA;

Query Match 91.3%; Score 105; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 0.00022; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 16; Conservative 16; DB 1; Mismatches 1; Indels 1; Gaps 0;
 Matches 1; DB 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GICRCCTRGRCIGCR 18
 Db 1 GICRCCTRGRCIGCR 18

RESULT 4
 ID AAE33866 standard; peptide: 18 AA.
 XX
 AC AAE33866;
 AC
 XX
 DT 16-APR-2003 (first entry)
 DE Macaca mulatta RTD1 peptide.
 XX
 KW Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV;
 KW human immunodeficiency virus; bacterial vaginosis; ophthalmic infection;
 KW antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A;
 KW RTD1.
 XX
 OS Macaca mulatta.
 OS
 XX Synthetic.
 XX
 FH Key FT Location/Qualifiers
 FT Modified-site 1..18
 FT /notes= "The peptide is cyclised by a covalent link
 between these two residues"
 FT Disulfide-bond 3..16
 FT Disulfide-bond 5..14
 FT Disulfide-bond 7..12
 XX
 PN US2004014669-A1.
 XX
 PD 22-JAN-2004.
 XX
 PR 30-APR-2003; 2003US-00427715.
 XX
 PR 30-APR-2002; 2002US-0377071P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Selsted ME, Tran DQ;
 XX
 DR WPI; 2004-167945/16.
 XX
 PT Novel theta defensin analog useful for reducing or inhibiting growth or
 PT survival of a microorganism in an environment such as food or food
 PT product, contact lens solution, or eye wash solution, an inanimate
 PT object.
 XX
 PS Claim 1; SEQ ID NO 29; 46pp; English.
 XX
 CC The invention relates to a theta defensin analogue defined by formulae
 CC detailed in the claims or appearing as ADO3239-AD035257. The theta
 CC defensin analogue is useful for reducing or inhibiting growth or survival
 CC of a microorganism in an environment capable of sustaining the growth or
 CC survival of the microorganism and is useful for reducing or inhibiting growth or
 CC survival of a microorganism in an environment such as food or
 CC food product, a solution (e.g., contact lens solution, or eye wash
 CC solution), an inanimate object comprising surface, or a mammal. The
 CC peptides are also useful for decreasing inflammatory response and for
 CC microbial inhibition of survival of microorganism as well as
 CC microbialistic inhibition of growth. Thus the peptides are useful as
 CC therapeutic agents, disinfectants, food preservatives, or medicaments.
 CC The peptides are also useful for treating a patient suffering from
 CC bacterial, viral, fungal or other infection. The theta defensins have
 CC high antimicrobial activity and low haemolytic activity. The present
 CC sequence represents a Rhesus theta defensin analogue peptide.

Query Match 90.4%; Score 104; DB 6; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00027; 1; Mismatches 2; Indels 1; Gaps 0;
 Matches 15; Conservative 15; DB 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GICRCCTRGRCIGCR 18
 Db 1 GICRCCTRGRCIGCR 18

RESULT 5
 ID ADO35255 standard; peptide: 18 AA.
 XX
 AC ADO35255;
 XX
 DT 15-JUL-2004 (first entry)
 DE Rhesus theta defensin analogue peptide RTD-4.
 XX
 KW Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial;
 KW antifungal; antibacterial; virucide; fungicide; food;
 KW contact lens solution; eye wash solution; inflammatory response;
 KW microbial inhibition; microbial growth inhibition; disinfectant;
 KW food preservative; bacterial infection; viral infection;
 KW fungal infection; haemolytic activity; cyclic.
 XX
 OS Macaca mulatta.
 OS
 XX Synthetic.
 XX
 FH Key FT Location/Qualifiers
 FT Modified-site 1..18
 FT /notes= "The peptide is cyclised by a covalent link
 between these two residues"
 FT Disulfide-bond 3..16
 FT Disulfide-bond 5..14
 FT Disulfide-bond 7..12
 XX
 PN US2004014669-A1.
 XX
 PD 22-JAN-2004.
 XX
 PR 30-APR-2003; 2003US-00427715.
 XX
 PR 30-APR-2002; 2002US-0377071P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Selsted ME, Tran DQ;
 XX
 DR WPI; 2004-167945/16.
 XX
 PT Novel theta defensin analog useful for reducing or inhibiting growth or
 PT survival of a microorganism in an environment such as food or food
 PT product, contact lens solution, or eye wash solution, an inanimate
 PT object.
 XX
 PS Claim 1; SEQ ID NO 29; 46pp; English.

CC The invention relates to a theta defensin analogue defined by formulae
 CC detailed in the claims or appearing as ADO3239-AD035257. The theta
 CC defensin analogue is useful for reducing or inhibiting growth or survival
 CC of a microorganism in an environment capable of sustaining the growth or
 CC survival of the microorganism and is useful for reducing or inhibiting growth or
 CC survival of a microorganism in an environment such as food or
 CC food product, a solution (e.g., contact lens solution, or eye wash
 CC solution), an inanimate object comprising surface, or a mammal. The
 CC peptides are also useful for decreasing inflammatory response and for
 CC microbial inhibition of survival of microorganism as well as
 CC microbialistic inhibition of growth. Thus the peptides are useful as
 CC therapeutic agents, disinfectants, food preservatives, or medicaments.
 CC The peptides are also useful for treating a patient suffering from
 CC bacterial, viral, fungal or other infection. The theta defensins have
 CC high antimicrobial activity and low haemolytic activity. The present
 CC sequence represents a Rhesus theta defensin analogue peptide.

CC spread within a virally-infected subject (VS), reducing viral burden in a VS, reducing virus shed from a VS, reducing percentage of VS in a population regardless of viral infection status, or inducing latency in a VS; (b) reducing the infectivity of a virus; and (c) rendering virus-contaminated tissue or fluid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (M1) is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered to a patient who is immunosuppressed or to a subject who is not infected with the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is chronically, latently or acutely infected with the virus. The present sequence represents a chimeric human/mouse monkey theta defense anti-viral peptide, which is given in the exemplification of the present invention.

XX SQ Sequence 18 AA:

Query Match	Score	DB	Length	Best Local Similarity	Pred. No.	Mismatches	Matches	Indels	Gaps
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1 GICRCICTRGFCRCIGR 18	100.0%	5	18	100.0%	2e-05	0	18	0	0

XX RESULT 2

ID	AAE33806	AC	AAE33806;	XX	DT	15-APR-2003	(first entry)
ID	AAE33806	AC	AAE33806;	XX	DT	15-APR-2003	(first entry)
ID	ADN08181	AC	ADN08181;	XX	DT	15-JUL-2004	(first entry)
ID	ADN08181	AC	ADN08181;	XX	DE	Human retrocyclin peptide, RC-105.	
ID	ADN08181	AC	ADN08181;	XX	KW	retrocyclin; cyclic; primate; retroviral infection; circular minidefense; retrocyclin; cyclic; antibacterial; virucide; vaccine; immunotherapy; microbial; viral; human.	
ID	ADN08181	AC	ADN08181;	XX	OS	Homo sapiens.	
ID	ADN08181	AC	ADN08181;	XX	OS	Synthetic.	
ID	ADN08181	AC	ADN08181;	XX	PN	WO2004033479-A2.	
ID	ADN08181	AC	ADN08181;	XX	PD	22-APR-2004.	
ID	ADN08181	AC	ADN08181;	XX	PP	06-MAY-2003; 2003WO-US014106.	
ID	ADN08181	AC	ADN08181;	XX	PR	06-MAY-2002; 2002US-0014645.	
ID	ADN08181	AC	ADN08181;	XX	PA	(RESC) UNIV CALIFORNIA.	
ID	ADN08181	AC	ADN08181;	XX	PA	(LEHR) LEHRER R I.	
ID	ADN08181	AC	ADN08181;	XX	PA	(WARI) WARING A J.	
ID	ADN08181	AC	ADN08181;	XX	PA	(COLE) COLE A M.	
ID	ADN08181	AC	ADN08181;	XX	PA	(HONG) HONG T B.	
ID	ADN08181	AC	ADN08181;	XX	PT	Lehrer RI, Waring AJ, Cole AM, Hong TB;	
ID	ADN08181	AC	ADN08181;	XX	DR	WPI; 2004-340883/31.	
ID	ADN08181	AC	ADN08181;	XX	PT	New isolated retrocyclin peptides and cyclic polypeptides, useful as therapeutic and prophylactic agents for treating and preventing microbial and viral infections.	
ID	ADN08181	AC	ADN08181;	XX	PR	18-APR-2001; 2001US-0284855P.	
ID	ADN08181	AC	ADN08181;	XX	PS	Claim 9; SEQ ID NO 6; 82pp; English.	
ID	ADN08181	AC	ADN08181;	XX	XX	The invention relates to a novel isolated retrocyclin peptide. The invention further provides: a cyclic polypeptide; an isolated nucleic acid encoding a primate retrocyclin; a method for preventing retroviral infection in a cell by administering an effective dose of a circular minidefense or retrocyclin to the cell; a method for killing microbial organisms by administering an effective dose of retrocyclin to the microbial organisms; a method for administering retrocyclin as a therapeutic agent to a patient with an established microbial or viral	
ID	ADN08181	AC	ADN08181;	XX	CC	transmitted diseases, vaginosis.	
ID	ADN08181	AC	ADN08181;	XX	CC	Claim 9; Page 24; 72pp; English.	

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OM protein - protein search, using sw model
Run on: March 22, 2005, 20:22:01 ; Search time 164 seconds
(without alignments)
42.449 Million cell updates/sec

Title: US-10-721-839-32
Perfect score: 115
Sequence: 1 GICRCICTRGFCRCICGR 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqP1990s;*
3: geneseqP2000s;*
4: geneseqP2001s;*
5: geneseqP2002s;*
6: geneseqP2003as;*
7: geneseqP2003bs;*
8: geneseqP2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

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AC	ABP5299;	
XX		
DT	13-NOV-2002	(first entry)
XX		
DE		Anti-viral chimeric theta defensin peptide H/RTD-2 SEQ ID NO:32.
KW		Anti-viral; viral infection; theta-defensin; lipid environment; amphiphatic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
XX		
OS		Macaca mulatta.
OS		Synthetic.
XX		
PN	WO200260468-A2.	
XX		
PD	08-AUG-2002.	
PP	29-JAN-2002; 2002WO-US002435.	
XX		
PR	30-JAN-2001; 2001US-0265270P.	
PR	01-AUG-2001; 2001US-0309368P.	
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PA	(IOWA) UNIV IOWA RES FOUND.	
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PT	Maury W, Stapleton J, Stinski M, Roller R, McCray PB, Tack B;	
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Abp5299 Anti-vira		
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Adn08181 Human retr		
Aae3866 Macaca mu		
Aae3866 Macaca mu		
Ado3255 Rhesus th		
Ado3255 Rhesus th		
Abp53046 Theta def		
Abp53295 Anti-vira		
Abp53295 Anti-vira		
Ado3230 Rhesus th		
Abp53294 Synthetic		
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Search time 141 Seconds
(without alignments)
42.197 Million cell updates/sec

On protein - protein search, using SW model

Run on: March 22, 2005, 20:46:53 ; Search time 141 Seconds

Title: US-10-721-839-32

Perfect score: 115

Sequence: 1 GICRCICTRGFCRCICGR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1401741

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	90.4	18 15	US-10-427-715-29	Sequence 32, Appli
5	89.6	18 14	US-10-060-102-28	Sequence 29, Appli
6	89.6	18 15	US-10-427-715-2	Sequence 28, Appli
7	89.6	18 15	US-10-427-715-14	Sequence 2, Appli
8	89.6	18 15	US-10-721-839-28	Sequence 28, Appli
9	88.7	18 14	US-10-060-102-27	Sequence 27, Appli
10	88.7	18 14	US-10-141-645-1	Sequence 1, Appli
11	88.7	18 15	US-10-721-839-27	Sequence 27, Appli
12	87.0	18 14	US-10-060-102-31	Sequence 31, Appli
13	87.0	18 15	US-10-721-839-31	Sequence 31, Appli

RESULT 1
US-10-060-102-32
; Sequence 32, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN DEFENSINS
TITLE OF INVENTION: CATHELICIDINS
FILE REFERENCE: IONA:031US
CURRENT APPLICATION NUMBER: US/10/060,102
PRIORITY FILING DATE: 2002-05-22
PRIORITY APPLICATION NUMBER: 601309,368
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1

; SBO ID NO: 32
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-10-060-102-32
Query Match 100.0%; Score 115; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GICRCICTRGFCRCICGR 18

Db 1 GICRCICTRGFCRCICGR 18
 RESULT 2
 US-10-721-839-32
 Sequence 32, Application US/10721839
 Publication No. US20040086535A1
 GENERAL INFORMATION:
 APPLICANT: MAURY, WENDY
 APPLICANT: STAPLETON, JACK
 APPLICANT: ROLLER, RICHARD
 APPLICANT: STINSKI, MARK
 APPLICANT: MCCRAY, PAUL B.
 TITLE OF INVENTION: NOVEL ANTI VIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
 TITLE OF INVENTION: CATHIELLICIDINS
 FILE REFERENCE: IOWA:035US
 CURRENT APPLICATION NUMBER: US/10/721,839
 CURRENT FILING DATE: 2003-11-25
 PRIOR APPLICATION NUMBER: US/10/060,102
 PRIOR FILING DATE: 2002-02-22
 PRIOR APPLICATION NUMBER: 60/309,368
 PRIOR FILING DATE: 2001-08-01
 PRIOR APPLICATION NUMBER: 60/265,270
 PRIOR FILING DATE: 2001-01-30
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 32
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-10-721-839-32
 Query Match 100.0%; Score 115; DB 15; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; MisMatches 0; Del 0; Insert 0;
 Qy 1 GICRCICTRGFCRCICGR 18
 Db 1 GICRCICTRGFCRCICGR 18
 RESULT 3
 US-10-721-839-32
 Sequence 6, Application US/10721839
 Publication No. US20040086535A1
 GENERAL INFORMATION:
 APPLICANT: Robert Lehrer
 APPLICANT: Alan Waring
 APPLICANT: Alexander Cole
 APPLICANT: Teresa Hong
 TITLE OF INVENTION: Retrecyclins - Antiviral and
 TITLE OF INVENTION: Antimicrobial Peptides
 FILE REFERENCE: UCLA-01CIP
 CURRENT APPLICATION NUMBER: US/10/141,645
 CURRENT FILING DATE: 2002-05-06
 PRIOR APPLICATION NUMBER: 60/284,855
 PRIOR FILING DATE: 2001-04-18
 PRIOR APPLICATION NUMBER: Unsigned
 PRIOR FILING DATE: 2002-04-18
 NUMBER OF SEQ ID NOS: 125
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 6
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic variant
 US-10-141-645-6
 Query Match 91.3%; Score 105; DB 14; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.3e-05; Mismatches 1; Indels 0; Gaps 0;
 Matches 16; Conservative 1; MisMatches 1; Del 0; Insert 0;
 Qy 1 GICRCICTRGFCRCICGR 18
 Db 1 GICRCICRGFCRCICGR 18
 RESULT 4
 US-10-427-715-29
 Sequence 29, Application US/10427715
 Publication No. US20040014669A1
 GENERAL INFORMATION:
 APPLICANT: Selsted, Michael E.
 APPLICANT: Tran, Dat Q.
 TITLE OF INVENTION: Thereof, and Methods of Use
 FILE REFERENCE: 65778-302 (US5754)
 CURRENT APPLICATION NUMBER: US/10/427,715
 CURRENT FILING DATE: 2003-04-30
 PRIOR APPLICATION NUMBER: US 60/377,071
 PRIOR FILING DATE: 2002-04-30
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 29
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic construct
 US-10-427-715-29
 Query Match 90.4%; Score 104; DB 15; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; MisMatches 0; Del 0; Insert 0;
 Qy 1 GICRCICTRGFCRCIC 16
 Db 1 GICRCICTRGFCRCIC 16
 RESULT 5
 US-10-060-102-28
 Sequence 28, Application US/10060102
 Publication No. US20030022829A1
 GENERAL INFORMATION:
 APPLICANT: MAURY, WENDY
 APPLICANT: STAPLETON, JACK
 APPLICANT: ROLLER, RICHARD
 APPLICANT: STINSKI, MARK
 APPLICANT: MCCRAY, PAUL B.
 APPLICANT: TACK, BRIAN
 TITLE OF INVENTION: NOVEL ANTI VIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
 TITLE OF INVENTION: CATHIELLICIDINS
 FILE REFERENCE: IOWA:035US
 CURRENT APPLICATION NUMBER: US/10/060,102
 CURRENT FILING DATE: 2002-02-22
 PRIOR APPLICATION NUMBER: 60/309,368
 PRIOR FILING DATE: 2001-08-01
 PRIOR APPLICATION NUMBER: 60/265,270
 PRIOR FILING DATE: 2001-01-30
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 28
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-10-060-102-28

Query Match 89.6%; Score 103; DB 14; Length 18;
 Best Local Similarity 88.9%; Pred. No. 3.8e-05; Length 18;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCRCICGR 18
 Db 1 GFRCRICTRGFCRCICTR 18

RESULT 6 US-10-427-715-2
 sequence 2, Application US/10427715
 Publication No. US20040014669A1
 GENERAL INFORMATION:
 APPLICANT: Sjelstad, Michael E.
 APPLICANT: Tran, Dat Q.
 TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
 TITLE OF INVENTION: Thereof, and Methods of Use
 FILE REFERENCE: 66778-302(UC5754)
 CURRENT APPLICATION NUMBER: US10/427,715
 CURRENT FILING DATE: 2003-04-30
 PRIOR APPLICATION NUMBER: US 60/377,071
 PRIOR FILING DATE: 2002-04-30
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 18
 TYPE: PRT
 ORGANISM: MACACA MULATTA

US-10-427-715-2

Query Match 89.6%; Score 103; DB 15; Length 18;
 Best Local Similarity 88.9%; Pred. No. 3.8e-05; Length 18;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCRCICGR 18
 Db 1 GFRCRICTRGFCRCICTR 18

RESULT 7 US-10-427-715-14
 Sequence 14, Application US/10427715
 Publication No. US20040014669A1
 GENERAL INFORMATION:
 APPLICANT: Sjelstad, Michael E.
 APPLICANT: Tran, Dat Q.
 TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
 TITLE OF INVENTION: Thereof, and Methods of Use
 FILE REFERENCE: 66778-302(UC5754)
 CURRENT APPLICATION NUMBER: US10/427,715
 CURRENT FILING DATE: 2003-04-30
 PRIOR APPLICATION NUMBER: US 60/377,071
 PRIOR FILING DATE: 2002-04-30
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 14
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic construct

US-10-427-715-14

Query Match 89.6%; Score 103; DB 15; Length 18;
 Best Local Similarity 88.9%; Pred. No. 3.8e-05; Length 18;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCRCICGR 18
 Db 1 GFRCRICTRGFCRCICTR 18

RESULT 8 US-10-721-839-28
 Sequence 28, Application US/10721839
 Publication No. US20040086535A1
 GENERAL INFORMATION:
 APPLICANT: Maury, Wendy
 APPLICANT: STAPLETON, JACK
 APPLICANT: ROLLER, RICHARD
 APPLICANT: STINSKI, MARK
 APPLICANT: MCCRAY, PAUL B.
 TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN DEFENSINS
 TITLE OF INVENTION: CATHELICIDINS
 FILE REFERENCE: IONA:031US
 CURRENT APPLICATION NUMBER: US10/721,839
 CURRENT FILING DATE: 2003-11-25
 PRIOR APPLICATION NUMBER: US10/050,102
 PRIOR FILING DATE: 2002-02-22
 PRIOR APPLICATION NUMBER: 60/309,368
 PRIOR FILING DATE: 2001-08-01
 PRIOR APPLICATION NUMBER: 60/265,270
 PRIOR FILING DATE: 2001-01-30
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 28
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide

US-10-721-839-28

Query Match 89.6%; Score 103; DB 15; Length 18;
 Best Local Similarity 88.9%; Pred. No. 3.8e-05; Length 18;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCRCICGR 18
 Db 1 GFRCRICTRGFCRCICTR 18

RESULT 9 US-10-050-102-27
 Sequence 27, Application US/10060102
 Publication No. US20030022829A1
 GENERAL INFORMATION:
 APPLICANT: MAURY, WENDY
 APPLICANT: STAPLETON, JACK
 APPLICANT: ROLLER, RICHARD
 APPLICANT: STINSKI, MARK
 APPLICANT: MCCRAY, PAUL B.
 APPLICANT: TACK, BRIAN
 TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN DEFENSINS
 TITLE OF INVENTION: CATHELICIDINS
 FILE REFERENCE: IONA:031US
 CURRENT APPLICATION NUMBER: US10/060,102
 CURRENT FILING DATE: 2002-02-22
 PRIOR APPLICATION NUMBER: 60/309,368
 PRIOR FILING DATE: 2001-08-01
 PRIOR APPLICATION NUMBER: 60/265,270
 PRIOR FILING DATE: 2001-01-30
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 27
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Pepsite
 OTHER INFORMATION: Pepsite

US-10-050-102-27

Query Match 88.7%; Score 102; DB 14; Length 18;
 Best Local Similarity 88.9%; Pred. No. 4.9e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCRCICGR 18
 Db 1 GICRCICRGRCICGR 18

RESULT 10
 US-10-141-645-1
 Sequence 1, Application US/10141645
 Publication No. US20030144184A1
 GENERAL INFORMATION:
 APPLICANT: Robert Lehrer
 APPLICANT: Alan Waring Cole
 APPLICANT: Teresa Hong
 TITLE OF INVENTION: Retrocyclins - Antiviral and
 TITLE OF INVENTION: Antimicrobial Peptides
 FILE REFERENCE: UCL-A-01CIP
 CURRENT APPLICATION NUMBER: US/10/141,645
 CURRENT FILING DATE: 2002-05-06
 PRIORITY APPLICATION NUMBER: 60/284,855
 PRIOR FILING DATE: 2001-04-18
 PRIOR APPLICATION NUMBER: Unassigned
 PRIORITY FILING DATE: 2002-04-18
 NUMBER OF SEQ ID NOS: 125
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-141-645-1

Query Match 88.7%; Score 102; DB 14; Length 18;
 Best Local Similarity 88.9%; Pred. No. 4.9e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCRCICGR 18
 Db 1 GICRCICRGRCICGR 18

RESULT 11
 US-10-721-839-27
 Sequence 27, Application US/10721839
 Publication No. US20040086535A1
 GENERAL INFORMATION:
 APPLICANT: MAURY, WENDY
 APPLICANT: STAPLETON, JACK
 APPLICANT: ROLLER, RICHARD
 APPLICANT: STINSKI, MARK
 APPLICANT: MCCRAY, PAUL B.
 APPLICANT: TACK, BRIAN
 TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
 FILE REFERENCE: IOWA:035US
 CURRENT APPLICATION NUMBER: US/10/060,102
 CURRENT FILING DATE: 2002-02-22
 PRIORITY APPLICATION NUMBER: 60/309,368
 PRIOR FILING DATE: 2001-08-01
 PRIORITY APPLICATION NUMBER: 60/265,270
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 31
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-10-060-102-31

Query Match 87.0%; Score 100; DB 14; Length 18;
 Best Local Similarity 83.3%; Pred. No. 8.2e-05; Mismatches 1; Indels 0; Gaps 0;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCRCICGR 18
 Db 1 GICRCICRGVCRCICGR 18

RESULT 13
 US-10-721-839-31
 Sequence 31, Application US/10721839
 Publication No. US20040086535A1
 GENERAL INFORMATION:
 APPLICANT: MAURY, WENDY
 APPLICANT: STAPLETON, JACK
 APPLICANT: ROLLER, RICHARD
 APPLICANT: STINSKI, MARK
 APPLICANT: MCCRAY, PAUL B.
 APPLICANT: TACK, BRIAN
 TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
 FILE REFERENCE: IOWA:035US
 CURRENT APPLICATION NUMBER: US/10/721,839
 CURRENT FILING DATE: 2003-11-25
 PRIORITY APPLICATION NUMBER: 60/309,368
 PRIOR FILING DATE: 2001-08-01
 PRIORITY APPLICATION NUMBER: 60/265,270
 PRIOR FILING DATE: 2001-01-30
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 27
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence

; PRIOR FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: 60/265,270
 ; PRIOR FILING DATE: 2001-01-30
 ; NUMBER OF SEQ ID NOS.: 32
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 31
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 ; US-10-721-839-31

Query Match 87.0%; Score 100; DB 15; Length 18;
 Best local Similarity 83.3%; Pred. No. 8.2e-05; 2; Indels 0; Gaps 0;
 Matches 15; Conservative 1; Mismatches 2;

Qy	Db	Sequence
1	1	GICRCICTGFCRCCIGR 18 :
		GICRCLLCRRCVGRCIGR 18

RESULT 14

US-10-141-645-2
 ; Sequence 2, Application US/10141645
 ; Publication No. US20030144184A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert Lehrer
 ; APPLICANT: Alan Waring
 ; APPLICANT: Alexander Cole
 ; APPLICANT: Teresa Hong
 ; TITLE OF INVENTION: Retrocyclins - Antiviral and
 ; FILE REFERENCE: UCLA-001CP
 ; CURRENT APPLICATION NUMBER: US/10/141,645
 ; CURRENT FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: 60/284,855
 ; PRIOR FILING DATE: 2001-04-18
 ; PRIOR APPLICATION NUMBER: Unsigned
 ; PRIOR FILING DATE: 2002-04-18
 ; NUMBER OF SEQ ID NOS: 125
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic variant
 ; US-10-141-645-2

Query Match 87.0%; Score 100; DB 15; Length 18;
 Best local Similarity 83.3%; Pred. No. 8.2e-05; 2; Indels 0; Gaps 0;
 Matches 15; Conservative 1; Mismatches 2;

Qy	Db	Sequence
1	1	GICRCICTGFCRCCIGR 18 :
		GICRCLLCRRCVGRCIGR 18

Search completed: March 22, 2005, 21:02:08
 Job time : 144 secs

; CURRENT FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: 60/284,855
 ; PRIOR FILING DATE: 2001-04-18
 ; PRIOR APPLICATION NUMBER: Unsigned
 ; NUMBER OF SEQ ID NOS: 125
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 18
 ; TYPE: RT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic variant
 ; US-10-141-645-3

Query Match 84.3%; Score 97; DB 14; Length 18;
 Best Local Similarity 83.3%; Pred. No. 0.00018; 3; Mismatches 0;
 Matches 15; Conservative 1; Indels 0; Gaps 0;
 Number of Seq ID Nos: 125

Qy	Db	Sequence
1	1	GICRCICTGFCRCCIGR 18 :
		GICRCYCGRGICRCIGR 18

RESULT 15

US-10-141-645-3
 ; Sequence 3, Application US/10141645
 ; Publication No. US20030144184A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert Lehrer
 ; APPLICANT: Alan Waring
 ; APPLICANT: Alexander Cole
 ; APPLICANT: Teresa Hong
 ; TITLE OF INVENTION: Retrocyclins - Antiviral and
 ; TITLE OF INVENTION: Retrocyclins - Antiviral and
 ; TITLE OF INVENTION: Antimicrobial Peptides
 ; FILE REFERENCE: UCLA-001CP
 ; CURRENT APPLICATION NUMBER: US/10/141,645

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Om protein - protein search, using sw model
GenCore version 5.1.6

ALIGNMENTS

hypothetical prote
 hypothetical prote
 high cysteine chor
 hypothetical prote
 fibrillin I - bovi
 fibrillin-1 precur
 fibrillin 1 precur
 metallothionein A
 metallothionein A
 proteinase inhibit
 proteinase inhibit
 proteinase inhibit
 proteinase inhibit
 proteinase inhibit
 hypothetical prote
 omega-conotoxin re
 tional protein

F;21-64/Domain: amino-terminal propeptide #status predicted <PRO>
F;74-76/Domain: carboxyl-terminal propeptide #status predicted <C-terminus>

Query Match 55.7%; Score 64; DB 2; Length 76;
Best Local Similarity 83.3%; Pred. No. 0/23; 1; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RCICCTRGFCRCI 15
Db 65 RCICCTRGFCRL 76

RESULT 3

E71602 probable integral membrane protein PFB0950w - malaria parasite (*Plasmodium falciparum*)

C;Species: *Plasmodium falciparum* #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004

C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004

R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;

R;Pertelet, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.

A;Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.

A;Reference number: A71600; MUID:99021743; PMID:9804551

A;Accession: E71602
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Experimental source: strain Bristol N2; clone C27a2
A;Genetics: C;Species: *Caenorhabditis elegans*

A;Accession: C27A2.5
A;Gene: CESP:C27A2.5

A;Map position: 2
A;Introns: 19/3; 91/2

Query Match 50.0%; Score 57.5; DB 2; Length 248;
Best Local Similarity 66.7%; Pred. No. 3; Mismatches 0; Indels 2; Gaps 3; Matches 10; Conservative 10; Mismatches 0; Indels 3; Gaps 1;

Qy 2 ICRCCTRGFCRCI 16
Db 162 ICSCICT--CRCIC 173

RESULT 4

T24272 hypothetical protein T01B7.8 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans* #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T24272
R;Simberg, M.
submitted to the EMBL Data Library, October 1995

A;Reference number: Z19867
A;Accession: T24272

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA
A;Residues: 1-154 <WIL>

A;Cross-references: UNIPROT:Q22048; EMBL:266499; PIDN:CAA91301.1; GSPDB:GN00020; CESP:T01B7.8

A;Experimental source: clone T01B7
A;Genetics: C;Genetics:
A;Map position: 2
A;Introns: 20/3; 90/2

Query Match 44.3%; Score 51; DB 2; Length 164;
Best Local Similarity 50.0%; Pred. No. 14; Mismatches 9; Indels 0; Gaps 0; Matches 9; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCHCICGR 18
Db 80 GCGCCCCCRPRCCCCRR 97

RESULT 5
T15651 hypothetical protein C27A2.5 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans* #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T15651
R;Nhan, M.
Submitted to the EMBL Data Library, May 1996

A;Description: The sequence of *C. elegans* coomid C27A2.

A;Reference number: Z18382
A;Accession: T15651

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA
A;Residues: 1-188 <WHA>

A;Cross-references: UNIPROT:Q182238; EMBL:U58760; PIDN:91330394; PIDN:9133039; PIDN:AAB0071

Query Match 44.3%; Score 51; DB 2; Length 188;
Best Local Similarity 50.0%; Pred. No. 15; Mismatches 9; Indels 0; Gaps 0; Matches 9; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GICRCICTRGFCHCICGR 18
Db 81 GCGCCCCCRPRCCCCRR 98

RESULT 6
S32834 methylviologen-reducing hydrogenase chain vncG [similarity] - *Methanococcus voltae*

C;Species: *Methanococcus voltae* #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C;Accession: S32834; S16726
R;Klein, A.
submitted to the EMBL Data Library, August 1991

A;Reference number: S32833
A;Accession: S32834
A;Status: Preliminary

A;Molecule type: DNA
A;Residues: 1-106 <KLE>

A;Cross-References: UNIPROT:Q00406; EMBL:X61203; PIDN:9296614; PIDN:CAA43505.1; PIDN:929661

R;Halboth, S.; Klein, A.
submitted to the EMBL Data Library, August 1991

A;Description: *Methanococcus voltae* harbors two gene groups each of homologous (NtFe) - ar

A;Reference number: S16721
A;Accession: S16726

A;Molecule type: DNA
A;Residues: 1-99, 'TA', 102-107, 'P', 126, 'LH', 129-306 <HAL>

A;Cross-references: EMBL:X61203
A;Note: the sequence is revised in GenBank entry X61203, release 117, (PIDN:CAA43505.1)

R;Halboth, S.; Klein, A.
Mol. Gen. Genet. 233, 217-224, 1992

A;Title: *Methanococcus voltae* harbors four gene clusters potentially encoding two [NtFe]

A;Reference number: A59304; MUID:92293118; PMID:1603063

A;Contents: annotation
C;Genetics:

A;Gene: vncG
C;Superfamily: methyl viologen-reducing hydrogenase gamma chain

Query Match 44.3%; Score 51; DB 2; Length 306;
Best Local Similarity 46.7%; Pred. No. 21; Mismatches 6; Indels 0; Gaps 0; Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ICRCICTRGFCHCICGR 16
Db 214 VCGVATRASRCFC 228

RESULT 7
S58870 reelin precursor - mouse

C;Species: *Mus musculus* (house mouse)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 21-Jul-2003

RESULT 5
T15651 hypothetical protein C27A2.5 - *Caenorhabditis elegans*

C;Accession: S58870; S71844; 149297
 R;D;Arcangelo, G.; Miao, G.G.; Chen, S.C.; Soares, H.D.; Morgan, J.I.; Curran, T.
 Nature 374, 719-723, 1995
 A;Title: A protein related to extracellular matrix proteins deleted in the mouse mutant
 A;Reference number: 149297; MUID:95231649; PMID:7715726
 A;Accession: S58870
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-3461 <DAR>
 A;Cross-references: EMBL:U24703; NID:9902486; PID:9902487
 R;D;Arcangelo, G.
 submitted to the EMBL Data Library, April 1995
 A;Reference number: S71844
 A;Accession: S71844
 A;Molecule type: mRNA
 A;Residues: 1-215, 'T', 217-1905, 'S', 1907-3355, 'V', 3357-3391, 'N', 3393-3461 <DA2>
 A;Cross-references: EMBL:U24703; NID:9902487; PID:9902487
 F;28-3461/Product: reelin #status predicted <MAT>
 Query Match 43.9%; Score 50.5; DB 2; Length 3461;
 Best Local Similarity 52.6%; Pred. No. 1.3e+02;
 Matches 10; Conservative 1; Mismatches 5; Indels 3; Gaps 1;
 Qy 1 GIC---RCIICTRGFCRCIC 16
 Db 1777 GICDSGRCVDRGFGPFC 1795

RESULT 8
 JCS677
 RNA4 protein - Beet necrotic yellow vein mosaic virus
 C;Species: Beet necrotic yellow vein mosaic virus
 C;Date: 11-Nov-1997 #sequence_revision 11-Nov-1997 #text_change 09-Jul-2004
 C;Accession: JCS677
 R,Yu, J.L.; Han, C.G.; Yan, L.L.; Li, D.W.; Liu, Y.
 Acta Microbiol. Sin. 37, 7-14, 1997
 A;Title: cDNA cloning, sequence analysis and expression of RNA4 from beet necrotic yellid
 A;Reference number: JCS677
 A;Accession: JCS677
 A;Molecule type: mRNA
 A;Residues: 1-282 <YUA>
 A;Cross-references: UNIPROT:Q65670

Query Match 43.0%; Score 49.5; DB 2; Length 282;
 Best Local Similarity 42.1%; Pred. No. 30;
 Matches 8; Conservative 1; Mismatches 5; Indels 5; Gaps 1;
 Qy 5 CICTRGPC---RCICGR 18
 Db 183 CVCAGSGCVFNDNHCFCGR 201

RESULT 9
 TMB
 trypsin inhibitor (Bowman-Birk) - mung bean
 C;Species: Vigna radiata (mung bean)
 C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
 C;Accession: A01301
 R,Zhang, Y.; Luo, S.; Tan, F.; Qi, Z.; Xu, L.; Zhang, A.
 Sci. Sin. 25, 268-277, 1982
 A;Title: Complete amino acid sequence of mung bean trypsin inhibitor.
 A;Reference number: A01301
 A;Accession: A01301
 A;Molecule type: protein
 A;Residues: 1-72 <ZHA>
 A;Cross-references: UNIPROT:P01062
 A;Note: three isoforms are also found whose amino ends differ slightly from that sh
 C;Comment: This inhibitor stoichiometrically inhibits trypsin in a molar ratio of 1:2.
 C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
 C;Keywords: duplication; serine proteinase inhibitor

RESULT 10
 JC1066
 trypsin inhibitor - mung bean
 C;Species: Vigna radiata (mung bean)
 C;Date: 02-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 18-Aug-2000
 C;Accession: JC1066
 R,Chen, C.Q.; Mao, J.P.; Zhang, M.F.; Dai, J.F.
 Chinese J. Biotechnol. 9, 54-60, 1993
 A;Title: Synthesis of mung bean trypsin inhibitor by the combination of the single strand
 A;Reference number: JC1066
 A;Accession: JC1066
 A;Molecule type: DNA
 A;Residues: 1-73 <CHE>
 C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
 F;2-73/Product: trypsin inhibitor #status predicted <MAT>
 F;41-40/Domain: Bowman-Birk inhibitor repeat homology <BB1>
 F;41-66/Domain: Bowman-Birk inhibitor repeat homology <BB12>
 Query Match 42.6%; Score 49; DB 2; Length 73;
 Best Local Similarity 58.8%; Pred. No. 14;
 Matches 10; Conservative 8; Mismatches 1; Indels 4; Gaps 2;
 Qy 3 CR-CICTR--GFRCI 15
 Db 441 CKSCICTRSMPGKCRCL 57

RESULT 11
 S08167
 Balbiani ring 3 protein - midge (Chironomus tentans)
 C;Species: Chironomus tentans
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-2004
 C;Accession: S08167
 R;Paulsson, G.; Lendahl, U.; Galli, J.; Ericsson, C.; Wieslander, L.
 J. Mol. Biol. 211, 331-349, 1990
 A;Title: The balbiani ring 3 gene in Chironomus tentans has a diverged repetitive structure
 A;Reference number: S08167; MUID:90172404; PMID:1689777
 A;Accession: S08167
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-1700 <PAU>
 A;Cross-references: UNIPROT:Q03376; GB:X52263; NID:97057; PIDN:CAA36506.1; PID:97058
 C;Genetics:
 A;Gene: BR3
 A;Map position: 4

Query Match 42.6%; Score 49; DB 2; Length 1700;
 Best Local Similarity 23.3%; Pred. No. 1.2e+02;
 Matches 7; Conservative 4; Mismatches 3; Indels 16; Gaps 1;
 Qy 3 CRCICTRG-----FCRCI 16
 Db 1245 CRCVCPKMKPADNCKTNDEMCOVCV 1274

RESULT 12
 T22945

hypothetical protein T01D3.1 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #text_change 03-Jul-2004
 C;Accession: T22345; T24295
 R;Percy, C.
 A;Reference number: Z19640
 A;Accession: T22345
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-3191 <WIL>
 A;Cross-references: UNIPROT:Q01135; EMBL:281094; PIDN:CAB03155.1; GSPDB:GN00023; CESP:T01D3.1
 A;Map position: 5
 A;Introns: 18/1; 73/2; 101/3; 241/2; 251/1; 327/3; 383/3; 455/3; 494/1; 793/1; 905/3; 10
 Query Match 42.2%; Score 48.5; DB 2; Length 83;
 Best Local Similarity 60.0%; Pred. No. 17; Mismatches 2; Indels 3; Gaps 1;
 Matches 9; Conservative 1; Mismatches 1; Indels 2; Gaps 2;
 C;Species: Glycine max (soybean)
 C;Accession: S07405; S29608; S40113
 R;Joudrier, P.E.; Foard, D.E.; Floener, L.A.; Larkins, B.A.
 Plant Mol. Biol. 10, 35-42, 1987
 A;Title: Isolation and sequence of cDNA encoding the soybean protease inhibitors PI IV a
 A;Accession: S07405
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-83 <JOU>
 A;Cross-references: UNIPROT:P01063; EMBL:M20732; NID:g169944; PIDN:AAA33953.1; PID:g1699
 A;Note: the sequences of codons 8-13 and 14-27 are interchanged in the authors' translat
 R;Baek, J.M.; Kim, S.I.
 submitted to the EMBL Data Library, October 1992
 A;Description: Nucleotide sequence of a cDNA encoding the soybean Bowman-Birk proteinase
 A;Reference number: S29559
 A;Accession: S29608
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-83 <BAE>
 A;Cross-references: EMBL:X66705; NID:g18567; PIDN:CAA48656.1; PID:g18568
 R;Giordano, A.; Deledone, M.; Fogher, C.; Marchetti, S.
 submitted to the EMBL Data Library, December 1993
 A;Description: Nucleotide sequence encoding a soybean C-II proteinase inhibitor.
 A;Reference number: S40113
 A;Accession: S40113
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-83 <GIO>
 A;Cross-references: EMBL:X76727; NID:g436413; PIDN:CAA54144.1; PID:g436414
 C;Superfamily: Bowman-Birk protease inhibitor; Bowman-Birk inhibitor repeat homology
 C;Keywords: serine proteinase inhibitor
 F;22-48/Domain: Bowman-Birk inhibitor repeat homology <BB1>

F;49-74/Domain: Bowman-Birk inhibitor repeat homology <BB12>
 C;Species: Glycine max (soybean)
 C;Date: 28-Aug-1985 #text_change 07-Oct-1994 #text_change 18-Aug-2000
 C;Accession: JC2225
 R;Baek, J.M.; Song, J.C.; Choi, Y.D.; Kim, S.I.
 Biosci. Biotechnol. Biochen. 58, 843-846, 1994
 A;Title: Nucleotide sequence homology of DNAs encoding soybean Bowman-Birk type protein
 A;Reference number: JCC224; MUID:94289861; PMID:7764974
 A;Accession: JC2225
 A;Molecule type: mRNA
 A;Residues: 1-94 <BAB>
 C;Genetics: This protein regulates endogenous proteinase during germination, stores sulf
 C;Species: Glycine max (soybean)
 C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
 C;Keywords: duplication; seed; serine proteinase inhibitor
 F;19-94/Domain: Signal Sequence #status predicted <SIG>
 F;33-55/Domain: Bowman-Birk inhibitor repeat homology <BB1>
 F;60-85/Domain: Bowman-Birk inhibitor repeat homology <BB12>
 Query Match 42.2%; Score 48.5; DB 2; Length 94;
 Best Local Similarity 60.0%; Pred. No. 18; Mismatches 2; Indels 3; Gaps 1;
 Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
 RESULT 15
 TSYC2
 C;Species: Glycine max (soybean)
 C;Accession: A22636; A0102
 R;Hammond, R.W.; Foard, D.E.; Larkins, B.A.
 J. Biol. Chem. 259, 9883-9890, 1984
 A;Title: Molecular cloning and analysis of a gene coding for the Bowman-Birk protease in
 A;Content: annotation
 R;Hammond, R.W.; Foard, D.E.; Larkins, B.A.
 J. Biol. Chem. 260, 7806, 1985
 A;Reference number: A92540
 A;Contents: erratum
 A;Accession: A22636
 A;Molecule type: DNA
 A;Residues: 1-103 <HAM>
 A;Cross-references: UNIPROT:P01063; GB:K01967; NID:g169942; PIDN:AAA33952.1; PID:g169943
 R;Odani, S.; Ikenaka, T.
 J. Biochem. 82, 1523-1531, 1977
 A;Title: Studies on soybean trypsin inhibitors. XI. Complete amino acid sequence of a so
 A;Reference number: A01302; MUID:78087480; PMID:599141
 A;Accession: A01302
 A;Molecule type: protein
 A;Residues: 28-103 <DNA>
 C;Comment: This protein inhibits trypsin, elastase, and chymotrypsin. The site of interac
 C;Superfamily: Bowman-Birk protease inhibitor; Bowman-Birk inhibitor repeat homology
 C;Keywords: duplication; seed; serine proteinase inhibitor

F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-30/Product: proteinase inhibitor (Bowman-Birk) C-II #status experimental <MAT>
F;42-58/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F;59-94/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;41-95, 42-57, 45-91, 47-55, 65-72, 69-84, 74-82/Dsulfide bonds: #status predicted
F;49/Inhibitory site: Ala (elastase) #status predicted
F;76/Inhibitory site: Arg (trypsin) #status experimental

Query Match 42.2%; Score 48.5; DB 1; Length 103;
Best Local Similarity 60.0%; Pred. No. 20; Mismatches 2; Indels 3; Caps 1;
Matches 9; Conservative 1; Mismatches 2; Indels 3; Caps 1;
QY 4 RCLCTR--GFCRCI 15
| | | | |||:
DB 71 RACTRSMPGCRCL 85

Search completed: March 22, 2005, 20:50:38
Job time : 48 secB

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GenCore version 5.1.6
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OM protein - protein search, using BW model
Run on: March 22, 2005, 20:23:06 ; Search time 173 Seconds
(without alignments)
53.280 Million cell updates/sec

Title: US-10-721-839-32

Perfect score: 115
Sequence: GICRCICTRGFCRCITCGR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

UniProt 03;*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	64	55.7	76	TDLA_MACMU
2	61.5	53.5	168	Q87BLB
3	58.5	50.9	83	Q7PQ24
4	58	50.4	168	Q8PBT4
5	58	50.4	168	Q8CH20
6	58	50.4	168	Q9D912
7	58	50.4	173	Q9D92
8	57.5	50.0	307	Q928Z
9	56.5	49.1	163	Q8VU20
10	55	47.8	146	Q7QBV4
11	55	47.8	1823	Q7PPR5
12	54.5	47.4	190	Q9UT23
13	54.5	47.4	307	Q9HUU3
14	54	47.0	193	Q8S6V3
15	54	47.0	201	Q62052
16	54	47.0	609	Q7QKX8
17	53.5	46.5	319	Q7SXVO
18	53	46.1	336	Q7PN9
19	53	46.1	657	Q7QXH8
20	53	46.1	1365	Q7RN8B
21	53	46.1	2871	Q7RN87
22	52.5	45.7	129	Q7PQ70
23	52.5	45.7	512	Q6R199
24	52.5	45.7	2809	Q7SN90
25	52.5	45.7	3008	Q6Q144
26	52	45.2	112	Q9U45
27	52	45.2	274	Q949G1
28	52	45.2	848	Q93U55
29	51.5	44.8	101	Q7YX02
30	51.5	44.8	118	Q8CCN2
31	51.5	44.8	131	Q9D261

RESULT 1	
ID	TDLA_MACMU
AC	FB2270; Q9TU01;
DT	25-OCT-2004 (Rel. 45, Created)
DT	25-OCT-2004 (Rel. 45, Last sequence update)
DE	theta defensin-1, subunit A precursor (RDP-1a) (Demidefensin 2).
GN	Name=RTDIA;
OS	Macaca mulatta (Rhesus macaque).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
OC	NCBI_TaxID:9544;
RN	[1] SEQUENCE FROM N.A., SEQUENCE OF 65-73, TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND DISULFIDE BONDS.
RC	TISSUE-Bone marrow, and Leukocyte;
RK	MEDLINE=99433140; PubMed=10521339; DOI=10.1126/science.286.5439.498;
RA	Tang Y.-O., Yuan J., Oesapay K., Tran D., Miller C.J., Ouellette A.J., Selsted M.E., Lehrer R.I.; "A cyclic antimicrobial peptide produced in primate leukocytes by the ligation of two truncated alpha-defensins"; Science 286:498-502 (1999).
RL	[2]
RN	SEQUENCE FROM N.A.
RC	TISSUE-Bone marrow;
RA	Zhao C., Nguyen T., Lehrer R.I.; "Lehrer R.I.; Submitted (SBP-1999) to the EMBL/GenBank/DDBJ databases.
RT	-I- FUNCTION: Active against the Gram-positive bacteria S.aureus and L.monocytogenes, Gram-negative bacteria S.typhimurium and E.coli
CC	M335 and fungi C.albicans and C.neoformans in vitro.
CC	-I- SUBUNIT: Forms a cyclic heterodimer composed of subunits A and B; disulfide-linked.
CC	-I- TISSUE SPECIFICITY: Expressed in bone marrow. Detected in promyelocytes, myelocytes and mature neutrophils and monocytes.
CC	-I- DEVELOPMENTAL STAGE: Expression begins early during Granulocyte myelopoiesis.
CC	-I- PTM: This is a cyclic peptide.
CC	-I- SIMILARITY: Belongs to the corticostatin/defensin family.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).
DR	EMBL; AF191100; AF043891.1; -.
DR	EMBL; AF184157; AF07924.1; -.

DR PIR: A59089; A59089.
 DR INTERPRO; IPR02366; Defensin_propep.
 DR Pfam; PF00379; Defensin_propep; 1.
 DR PROSITE; PS00269; DEFENSIN; FALSE_NSG.
 KW Antibiotic; Defensin; Direct protein sequencing; Fungicide; Signal.
 PT SIGNAL 1 22 Potential.
 PT PROPEP 23 64 Theta defensin-1, subunit A.
 PT PEPTIDE 65 73 Interchain (with C-66 of subunit B).
 PT PROPEP 74 76 DISULFID 66 66 PT DISULFID 68 73 T -> A (in Ref. 2).
 PT CONFLICT 38 38 SEQUENCE 76 AA; 8242 MW; BBA207932A030590 CRC64;
 Query Match 55.7%; Score 64; DB 1; Length 76;
 Best Local Similarity 83.3%; Pred. No. 0 47;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 4 RICCTRGRFCRCL 15 Db 65 RICCTRGRFCRCL 76
RESULT 2
 087BLB PRELIMINARY; PRT; 168 AA.
 ID 087BLB AC 087BLB DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=PD1431;
 OS Xylella fastidiosa (strain Temecula / ATCC 700964).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC NCBI_TAXID=183190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22421331; PubMed=12533478;
 RX DOI=10.1128/JB.185.3.1018-1026.2003;
 RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
 RA Miyaki C.Y., Furjan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
 RA Takita M.A., Lemos E.G.M., Macadamo M.A., Ferro M.I.T., da Silva F.R.,
 RA Goldman M.H.S., Goldmann G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,
 RA Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
 RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
 RA Marinho C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
 RA Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
 RA da Cunha A.P., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
 RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
 RA de Souza A.A., Truffi D., Tsukumo F., Yanei G.M., Zarcos L.G.,
 RA Civerolo E.L., Simpson A.J.G., Almeida N.P. Jr., Setubal J.C.,
 RA Kitajima J.P.;
 RT "Comparative analyses of the complete genome sequences of Pierce's
 disease and citrus variegated chlorosis strains of *Xylella*
 RT *fastidiosa*",
 RL J. Bacteriol. 185:1018-1026 (2003).
 DR EMBL; AE01558; AA029277.1; --.
 KW Complete proteome.
 SQ SEQUENCE 168 AA; 17967 MW; 87A2F5F3C5B818C9 CRC64;
 Query Match 53.5%; Score 61.5; DB 2; Length 168;
 Best Local Similarity 50.0%; Pred. No. 1 8; Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;
 Oy 1 GICRCICTRGRFCRIGR 18 Db 144 GVCCTCCVVRG--CVCGQ 15B
RESULT 3
 07PG24 PRELIMINARY; PRT; 83 AA.
 ID 07PG24 DR 07PG24 AC 07PG24
 DR INTERPRO; IPR02366; Defensin_propep.
 DR Pfam; PF00379; Defensin_propep; 1.
 DR PROSITE; PS00269; DEFENSIN; FALSE_NSG.
 KW Antibiotic; Defensin; Direct protein sequencing; Fungicide; Signal.
 PT SIGNAL 1 22 Potential.
 PT PROPEP 23 64 Theta defensin-1, subunit A.
 PT PEPTIDE 65 73 Interchain (with C-66 of subunit B).
 PT PROPEP 74 76 DISULFID 66 66 PT DISULFID 68 73 T -> A (in Ref. 2).
 PT CONFLICT 38 38 SEQUENCE 76 AA; 8242 MW; BBA207932A030590 CRC64;
 Query Match 55.7%; Score 64; DB 1; Length 76;
 Best Local Similarity 83.3%; Pred. No. 0 47;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 4 RICCTRGRFCRCL 15 Db 65 RICCTRGRFCRCL 76
RESULT 4
 06P8T4 PRELIMINARY; PRT; 168 AA.
 ID 06P8T4 AC 06P8T4 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE 493120D1Rik protein.
 GN Name=4931420D1Rik;
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TAXID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22428227; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX TISSUE=TESTIS;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Scheuer G.D.,
 RA Klausner R.D., Collins P.S., Wagner L., Sheinin C.M., Schuler N.G.,
 RA Aitschull S.F., Zeeberg B., Buston K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heilek F.,
 RA Ditchkenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schuetz T.E.,
 RA Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Kulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman J., Madden A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smilie D.E., Schenck A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences", Proc. Natl. Acad. Sci. U.S.A. 99:1689-16903 (2002).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Director MGC Project;
 RL Submitted (NOV-2003); to the EMBL/GenBank/DBJ databases.
 EMBL; BC061079; AAH61079.1; --.

SQ	SEQUENCE	168 AA;	18947 MW;	B00FD3D27B9BF768 CRC64;	RC
Query Match	50.4%; Score 58; DB 2;	Length 168;			STRAIN=C57BL/6J; TISSUE=Testis;
Best Local Similarity	56.2%; Pred. No. 5.1;				The FANTOM Consortium,
Matches	9; Conservative	0; Mismatches	7; Indels	0; Gaps	the RIKEN Genome Exploration
Oy	3 CRACTGFCRCCICGR 18				Research Group Phase I & II Team;
Db	66 CRCCCYCRCCRCSSR 81				Analysis of the mouse transcriptome based on functional annotation of
RESULT 5					
ID	08CH20	PRELIMINARY;	PRT;	168 AA.	RN
AC	08CH20;				RP
DT	01-MAR-2003 (TREMBrel. 23, Created)				RC
DT	01-MAR-2003 (TREMBrel. 23, Last sequence update)				RK
DT	01-JUN-2003 (TREMBrel. 24, Last annotation update)				RK
DB	Basic protein CKTR13				RK
GN	Name=g93142014Rik; Synonyms=Ckt1r3;				RK
OS	Mus musculus (Mouse)				RK
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				RK
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				RK
OK	NCBI_TaxID=10090;				RN
RN	[1] SEQUENCE FROM N.A.				RP
RC	STRAIN=CD-1; TISSUE=Testis;				RC
RA	Xu X., Silvius D., Escalier D., McFarland L., Xu P.-X.;				RC
RL	Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.				RC
DR	EMBL: AF463502; AA016751; -;				RC
DR	MGD: MGI:1913992; 4931420D14Rik.				RC
DR	SBSEQUENCE 168 AA; 18957 MW;	8F3003D27B9BF595 CRC64;			RC
Query Match	50.4%; Score 58; DB 2;	Length 168;			MDLINE=20530913; PubMed=1107681; DOI=10.1101/gr.152600;
Best Local Similarity	56.2%; Pred. No. 5.1;				Shibata K., Itoh M., Aizawa K., Nagakura S., Sasaki N., Carninci P.,
Matches	9; Conservative	0; Mismatches	7; Indels	0; Gaps	Konno H., Akiyama J., Nishi K., Kitamai T., Tashiro H., Itoh M.,
Oy	3 CRACTGFCRCCICGR 18				Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Marada A.,
Db	66 CRCCCYCRCCRCSSR 81				Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,
RESULT 6					
RP	SEQUENCE FROM N.A.				Yujikawa S., Inoue K., Togawa Y., Iwasa M., Ohara E., Watabiki M.,
RC	STRAIN=C57BL/6J; TISSUE=Testis;				Yoneda Y., Ishikawa T., Tanaka T., Matsuura S., Kawai J.,
RA	Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA	Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA	Hanagaki T., Hara A., Hayasawa N., Hiramoto K., Hirayama T., Hori F.,				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA	Imotani K., Ishii Y., Itoh M., Izawa M., Kasubata T., Kato H.,				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA	Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA	Matsuyama T., Mizraizaki A., Nishi K., Nomura K., Numasaki R., Ohno M.,				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA	Okazaki Y., Okido T., Owa S., Saito R., Sakai C., Sakai K.,				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA	Sano H., Saeki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA	Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA	Tejima Y., Toya T., Yamamoto T., Yasumishi A., Yoshida K., Yoshino M.,				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA	Muramatsu M., Hayashizaki Y.,				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RL	Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
DR	EMBL: AF06692; BAB24782.1; -;				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
DR	MGD: MGI:191392; 4931420D14Rik.				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
KW	Hypothetical protein.				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
SQ	SEQUENCE 168 AA; 18931 MW;	7A2BD279612A5E94 CRC64;			RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
Query Match	50.4%; Score 58; DB 2;	Length 168;			RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
Best Local Similarity	56.2%; Pred. No. 5.1;				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
Matches	9; Conservative	0; Mismatches	7; Indels	0; Gaps	RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
Oy	3 CRACTGFCRCCICGR 18				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
Db	66 CRCCCYCRCCRCSSR 81				RAizaki Y., Muranatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RESULT 7					
OPD4K2	PRELIMINARY;	PRT;	173 AA.		RC
OPD4K2					RA
AC	OPD4K2;				RA
DT	01-JUN-2001 (TREMBrel. 17, Created)				RT
DT	01-JUN-2001 (TREMBrel. 17, Last sequence update)				RT
DT	01-OCT-2002 (TREMBrel. 22, Last annotation update)				RT
DE	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931420D14 product:hypothetical Cysteine-rich region containing protein, full insert sequence.				DE
GN	Name=g433142014Rik;				DE
OS	Mus musculus (Mouse)				DE
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				DE
OX	NCBI_TaxID=10090;				DE
RN	SEQUENCE FROM N.A.				DE
RC	STRAIN=C57BL/6J; TISSUE=Testis;				DE
RA	Garnick P., Hayashizaki Y.,				DE
RA	"High-efficiency full-length cDNA cloning.";				DE
RL	Meth. Enzymol. 303:19-44(1999).				DE
RN	[2]				DE
RP	SEQUENCE FROM N.A.				DE
RC	STRAIN=C57BL/6J; TISSUE=Testis;				DE
RA	Medline=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)0004-9;				DE
RA	Garnick P., Hayashizaki Y.,				DE
RA	"High-efficiency full-length cDNA cloning.";				DE
RA	Medline=21085660; Pubmed=12171851; DOI=10.1038/35055500;				DE
RT	RIKEN FANTOM Consortium;				DE
RT	"Functional annotation of a full-length mouse cDNA collection.";				DE
RN	Nature 409:685-690(2001).				DE
RN	[3]				DE
SEQUENCE FROM N.A.					

[1] RESULT 8
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349336; DOI=10.1016/S0076-6879(99)03004-9;
 RA Garnicci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=1121751; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:1563-573 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20199374; PubMed=1042559; DOI=10.1101/gr.145100;
 RA Carnici P., Shibata K., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
 RA Kono H., Okaaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=1107661; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagioka S., Sasaki N., Carnicci P.,
 RA Kono H., Akiyama J., Nishi K., Kitunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura N., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujikawa S., Inoue K., Topawa Y., Irawa M., Ohara E., Watanuki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akaiwa S., Akimura T., Arai A., Aono H.,
 RA Arai T., Bono H., Carnicci P., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Ohno M.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R.,
 RA Okazaki Y., Okido T., Owa C., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shihata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 DR Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK01467; BAB31253.1; -.
 DR MGID: MGI:113992; 4931420D14Rik.
 KW Hypothetical protein
 SQ SEQUENCE 173 AA; 19581 MW; 147B6P155AC29FDP CRC64;

Query Match 50.4%; Score 58; DB 2; Length 173;
 Best Local Similarity 56.2%; Pred. No. 52; Mismatches 7; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

[1] RESULT 9
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349336; DOI=10.1016/S0076-6879(99)03004-9;
 RA Garnicci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=1121751; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:1563-573 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20199374; PubMed=1042559; DOI=10.1101/gr.145100;
 RA Carnici P., Shibata K., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
 RA Kono H., Okaaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=1107661; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagioka S., Sasaki N., Carnicci P.,
 RA Kono H., Akiyama J., Nishi K., Kitunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura N., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujikawa S., Inoue K., Topawa Y., Irawa M., Ohara E., Watanuki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akaiwa S., Akimura T., Arai A., Aono H.,
 RA Arai T., Bono H., Carnicci P., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Ohno M.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R.,
 RA Okazaki Y., Okido T., Owa C., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shihata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 DR Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK01467; BAB31253.1; -.
 DR MGID: MGI:113992; 4931420D14Rik.
 KW Hypothetical protein
 SQ SEQUENCE 173 AA; 19581 MW; 147B6P155AC29FDP CRC64;

Query Match 50.4%; Score 58; DB 2; Length 173;
 Best Local Similarity 56.2%; Pred. No. 52; Mismatches 7; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

[1] RESULT 9
 RP PRELIMINARY; PRT; 307 AA.
 AC 096282
 ID 096282
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DE Hypothetical protein PF80950w.
 GN Name=PF80950w;
 OS Plasmodium falciparum (Isolate 3D7).
 OC Baktaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 RN NCBI_TaxID=36329;
 RN [1]
 RP PRELIMINARY; PRT; 307 AA.
 RC 096282
 RX MEDLINE=99279253; PubMed=10349336; DOI=10.1016/S0076-6879(99)03004-9;
 RA Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
 RA Koorn E.V., Shallom S., Mason T., Yu K., Fujii C., Pedersen J.,
 RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Petrea M.,
 RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
 RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.,
 RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
 RT falciparum.";
 RL Science 282:1126-1132 (1998).
 RN [2]
 RP PRELIMINARY; PRT; 307 AA.
 RC 096282
 RX MEDLINE=99279253; PubMed=10349336; DOI=10.1016/S0076-6879(99)03004-9;
 RA Gardner M.J., Hall N., Rung E., White O., Beirimann M., Hyman R.W.,
 RA Carlson J.M., Pain A., Nelson K.E., Bowman I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyte S.,
 RA Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Anduoli S.,
 RA Perete M., Allen J., Selengut J., Haff D., Mater M.W., Vaidya A.B.,
 RA Martin D.M.A., Fairlamb M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.,
 RT "Genome sequence of the human malaria parasite Plasmodium
 RT falciparum.";
 RL Nature 419:498-511 (2002).
 DR EMBL: AE001428; AACT1979_2; -.
 DR PIR: ET1602; EI1602.
 DR HSSP: P01056; IH34.
 DR InterPro: IPR001368; TNFR_C6.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR Hypothetical protein.
 KW SEQUENCE 307 AA; 35537 MW; B95A3DB354D4BE71 CRC64;

Query Match 50.0%; Score 57.5; DB 2; Length 307;
 Best Local Similarity 66.7%; Pred. No. 9.6; Mismatches 2; Indels 3; Gaps 1;
 Matches 10; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

OY 2 ICRCICTRGFRCIC 16
 Db 221 ICSCICHT--CICIC 232

RESULT 9
 RP PRELIMINARY; PRT; 163 AA.
 ID 096282
 AC 096282
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusName=MN3454;
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Corynebacteriinae; Mycobacteriaceae; Mycobacterium;
 OC NCBI_TaxID=1773;
 RN [1]
 RP PRELIMINARY; PRT; 163 AA.
 RC 096282
 RX MEDLINE=22206494; PubMed=12218036;

RX DOI=10.1128/JB.184.19.5479-5490.2002;
 RA Fleischmann R.D., Alland D., Eshen J.A., Carpenter L., White O.,
 Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
 Hickey E.J., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
 Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khorri H.M.,
 Gill J., Mikula W., Jacobs W.R. Jr., Venter J.C.,
 Faber C.M., "Whole-genome comparison of *Mycobacterium tuberculosis* clinical and
 laboratory strains."; DR J. Bacteriol. 184:5479-5490 (2002).
 RL DR EMBL; AE005116; AAK47795.1; -.
 DR TIGR; MT3494; -.
 KW Hypothetical protein.
 SQ SEQUENCE 163 AA; 18621 MW; B5E62AB951B2AC3C CRC64;
 Query Match 49.1%; Score 56.5; DB 2; Length 163;
 Best Local Similarity 60.0%; Pred. No. 7.6;
 Matches 9; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
 Qy 3 CICCTCTR-GFCRCIC 16
 Db 137 CRHVCVTRSGYCRLLVC 151

RESULT 10

ID	Q7QBV4	PRELIMINARY;	PRT;	146 AA.
AC	Q7QBV4			
DT	01-MAR-2004	(TREMBLrel. 26, Created)		
DT	01-MAR-2004	(TREMBLrel. 26, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	AGCP194	(Fragment).		
GN	Name=qCG4401; ORFNAMES=ENSANGG0000012913;			
OS	Anopheles gambiae str. PEST.			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.			
OX	NBGI_TaxID=180454;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=PEST;			
RA	Anopheles Genome Sequencing Consortium; /DDBJ databases.			
RL	Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.			
CC	"CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data."			
DR	EMBL; AAB010847; BAA06054.2; -.			
DR	HSSP; P00740; IEMN.			
RT	InterPro; IPR00152; Asx_hydroxyl_S.			
RL	InterPro; IPR00985; ConA_like_lec_gly.			
DR	InterPro; IPR000742; EGF_2.			
DR	InterPro; IPR006209; EGF_1-like.			
DR	InterPro; IPR00930; Grow_fac_recept.			
DR	InterPro; IPR00310; Hyalin.			
DR	InterPro; IPR001791; Laminin_G.			
DR	InterPro; IPR01759; Pentaxin.			
DR	InterPro; IPR001211; PhospholipaseA2.			
DR	InterPro; IPR002335; VWF_A.			
DR	InterPro; IPR00088; EGF_5.			
PFAM	PF02094; HRV_R.			
PFAM	PF03554; Pentaxin_1.			
DR	PFAM; PF00034; Sushi_5.			
DR	PFAM; PF00092; VWA_1.			
DR	PRINTS; PRO0895; PENTAXIN.			
DR	PRINTS; PRO0453; WFADOMAIN.			
DR	PRODOM; PD002153; Pentaxin_1.			
DR	PROSITE; PS00010; ASK_HYDROXYL; UNKNOWN_1.			
DR	PROSITE; PS00022; EGF_1; UNKNOWN_5.			
DR	PROSITE; PS01186; EGF_2; 4.			
DR	PROSITE; PS00261; EGF_3; 5.			
DR	PROSITE; PS00825; HYR_2.			
DR	PROSITE; PS0025; LAM_G_DOMAIN; 1.			
DR	PROSITE; PS00116; PAI_HTS; UNKNOWN_1.			
DR	PROSITE; PS00923; SUSHI_8.			
DR	PROSITE; PS02034; VWF_A_1.			
PT	NON_TER	1	1	
FT	NON_TER	1823	1823	
SQ	SEQUENCE 1823 AA; 200582 MW; 5740C4C700804379 CRC64;			
Query Match 47.8%; Score 55; DB 2; Length 1823; Best Local Similarity 53.8%; Pred. No. 11; Gaps 0; Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;				
Qy 5 CICCTCTR-GFCRCIC 17 Db 44 CVCVTLGWCRCVGG 56				
ID	Q7PRP5	PRELIMINARY;	PRT;	1823 AA.
AC	Q7PRP5			
DT	01-MAR-2004	(TREMBLrel. 26, Created)		
DT	01-MAR-2004	(TREMBLrel. 26, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	ENSGANGG0000019046 (Fragment).			
GN	Name=ENSGANGG0000016557;			
OS	Anopheles gambiae str. PEST.			
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.			
OC	Neoptera; Metazoa; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.			
OX	NBGI_TaxID=180454;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
ID	Q8U123	PRELIMINARY;	PRT;	190 AA.
AC	Q8U123			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-OCT-2002	(TREMBLrel. 22, Last annotation update)		
DE	PRO0529.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NBGI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G.,			
RA	Zhang Y., Liu M., He F.,			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AR11848; RAF16687.1; -.			
DR	SEQUENCE 190 AA; 21480 MW; 4B810A29AA33844 CRC64;			

QY	2	ICRCICTRG---FCRCIC	16
Db	47	VCLCVCVRGCVSVCV	64
RESULT	13		
OCH93		PRELIMINARY;	PRT;
ID	QH93		PRT;
AC	QH93;		PRT;
DT	01-MAR-2001	(TREMBlrel. 16, Created)	
DT	01-MAR-2001	(TREMBlrel. 16, Last sequence update)	
DT	01-OCT-2002	(TREMBlrel. 22, Last annotation update)	
DE	Hypothetical protein	FLJ12547.	
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	PubMed=14702039; DOI=10.1038/ng1285;		
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyma T., Irie R., Wakamatsu M., Kanda K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shiba T., Tanaka T., Ishii S., Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagesuma M., Shiratori M., Sudo H., Hosobri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamiyama K., Katsuma N., Sato K., Tanaka M., Yamaoka M., Niromiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kinmata M., Watanaabe M., Hiraoka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanaabe S., Yosida M., Hotoda T., Kusano J., Kamehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togoya S., Konai F., Hara R., Takeuchi K., Arita M., Imose N., RA		
RA	Murasawa K., Yuuki H., Oshima A., Sasaki S., Yoshikawa Y., Matsumura H., Ichihara T., Shiohara N., Sano S., Moriya S., Monniyama H., Satoh N., Takami S., Terashima Y., Suzuki O., RA		
RA	Nakagawa S., Sano A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanaabe S., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Ohmori Y., RA		
RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Ochiai R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsunaga K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hatta H., Watanaabe M., Komatsu T., Takahashi T., Shiba T., Shiraishi Y., Nakagawa K., Mizushima-Sugano J., Satoh T., Shiraishi Y., Nakamura Y., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., RA		
RT	"Complete sequencing and characterization of 21,243 full-length human cDNAs"; Nat. Genet. 36:40-45(2004).		
RL	EMBL; AK022609; BAB1428.1; -.		
DR	SEQUENCE 307 AA; 32780 MW; 4CC18ACD39BD3AC3 CRC64;		
SQ	Query Match 47.4%; Score 54.5; DB 2; Length 307; Best Local Similarity 42.1%; Pred. No. 23; Matches 8; Conservative 3; Mismatches 5; Indels 3; Gaps 1; OY 2 ICRCICTRG---FCRCIC 17		
Db	100 VCAVCGCTFVCVCAVGCG 118		
RESULT	14		
OBS6V3		PRELIMINARY;	PRT;
ID	OBS6V3		PRT;
AC	OBS6V3;		PRT;
DT	01-JUN-2002	(TREMBlrel. 21, Created)	
DT	01-JUN-2002	(TREMBlrel. 21, Last sequence update)	
DT	01-JUL-2004	(TREMBlrel. 27, Last annotation update)	
DE	Hypothetical protein OSJNBa0014J14.16.		
DR	ORFnames=OSJNBa0014J14.16;		
RESULT	14		
OBS6V3		PRELIMINARY;	PRT;
ID	OBS6V3		PRT;
AC	OBS6V3;		PRT;
DT	01-JUN-2002	(TREMBlrel. 21, Created)	
DT	01-JUN-2002	(TREMBlrel. 21, Last sequence update)	
DT	01-JUL-2004	(TREMBlrel. 27, Last annotation update)	
DE	Hypothetical protein OSJNBa0014J14.16.		
Query Match 47.0%; Score 54; DB 2; Length 201; Best Local Similarity 40.0%; Pred. No. 19; Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0; OY 2 ICRCICTRGFCRCIC 16			
Db	58 VCLCVLVSVCVLCVC 72		

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Search completed: March 22, 2005, 20:49:45
Job time : 175 sec_B

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